

458 - - C^TGGCTGGCTAACCCAGTCAACTTCCAGCACGTTTACACTGTGAGG 513
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RESULT 4
5-08-92-126-114 Sequence 114 Application US/08592126
PATENT NO. 582091
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250

STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,126
FILING DATE:
CLASSIFICATION: 425
ATTORNEY/AGENT INFORMATION:
NAME: Shultz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880

TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0920
 INFORMATION FOR SEQ ID NO: 114:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 413 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA

MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: H505.seq
S-00-592125-1114

QY	510	GAGGGTAAACCATCTACTCAGCCCTAGCCTAGGCGATGACCTCTCCACCAAGCT	569
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QY	629	TCTTAAGTTGCTGGGTGCGTGGGG	653
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RESULT 5
US-09-168-595-114
Sequence 114, Application US/09168595

Patent No. 6555666
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Transcripts Encoding Immunomodulatory Polypeptides
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US 09/168,595
APPLICATION NUMBER: US 09/168,595

ACCESSION A0016709
 VERSION A0016709.T1 GI:3195445
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1. (bases 1 to 536)
 AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Goldin,B., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
 TITLE Use of random BAC End Sequence Database for Sequence-Ready Map Building (1998)
 JOURNAL Unpublished
 COMMENT Other GSSS: CIT-HSP-2301123.TF
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@tigr.org
 Clones are available from Research Genetics (info@researchgenetics.com). BAC end search page: http://www.tigr.org/tcb/hungen/bac_end_search.html.
 Seq primer: M13 Reverse Class: BAC ends.

FEATURES source
 Location/Qualifiers
 1. 536 /organism="Homo sapiens"
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 Matches 267; Conservative 0; Mismatches 50; Indels 1; Gaps 1;

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 Qy 265 TGTAGGGTCTCAGAGCTGATGGCTGGAGAATTCTGGGACTTCTTGTAGCTGTC 324
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 Qy 325 TGTCCCTGATATAGAGCTGATGGCTGGAGAATTCTGGGACTTCTTGTAGCTGTC 384
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 Db 280 AGGAGGGATGTTAACAGATGAGCTGAGTGATGGAGATCTGGCTCTCTAGAGTGGC 221
 Qy 445 CTGTCCTCGGGAGCTGTTG 462
 Db 220 CTGTCCTCGGGAGATGGG 203

DEFINITION DKFZp686D121186_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
 ACCESSION DKFZp686D121186_5 , mRNA sequence.
 BX476445 BX476445 1 GI:31673701
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 420)
 AUTHORS Koehler,K., Beyer,A., Newes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
 TITLE EST (Koehler,K., Beyer,A., Newes,H.W., Weil,B., Amid,C., et al.)
 JOURNAL Unpublished
 COMMENT Contact: Koehler K
 MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: wiemann@dkfz-heidelberg.de;
 sequenced by BMFZ (Biomedical Research Center at the Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. No s1 sequence available.
 This clone (DKFZp686D121186) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES source
 location/Qualifiers
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 BASE COUNT ORIGIN
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Query Match 12.7%; Score 220.6; DB 13; Length 420;
 Best Local Similarity 82.8%; Pred. No. 2.2e-35;
 Matches 264; Conservative 0; Mismatches 54; Indels 1; Gaps 1;

Qy 145 CGGAGGTGGAAACAAAGATTCGCTGTTCTACCTCTGGAGCTTGTCCAG 204
 Db 346 CAGGGCTGAGAACGAGATGCCGGAGAGCTCTCTGTATGGGTGTCAGCTGGAGCTTGTCCAG 287
 Qy 205 AAGGGACCCCGAGATGCCGGAGAGCTCTCCGTTATGGGTGTCGGCCCTAC 264
 Db 286 AGGGGACCCACCAAGATGCCAACAGGCTCTCCGTTATGGGTGTCGGCCCTAT 227
 Qy 325 TGTCCCTGATATAGAGCTGATGGCTGGAGAATTCTGGGACTTCTTGTAGCTGTC 384
 Db 385 AGGAGGGACGTTAACAGATGAGCTGAGTGATGGAGATCTGGCTCTCTAGAGTGGC 108
 Qy 445 CTGTCCTCGGGAGCTGTTG 463
 Db 47 CTGTCCTCGGGAGATGGGG 29

Search completed: October 31, 2003, 18:10:42
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